

SEQUENCE LISTING

<110> Castrillon, Diego H.

<120> COMPOSITIONS AND METHODS FOR THE IMPROVED DIAGNOSIS OF GERM CELL TUMORS

<130> B0801/7195/ERP/KA

<150> U.S. 60/166,394

<151> 1999-11-18

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<212> DNA

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2185

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Gly	Ser	Ser	Trp	Lys	Met	Thr	Gly	Asp	Ser	Phe	Arg	Gly	Arg	Gly	Gly
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Pro	Glu	Glu	Glu	Ser	Ser	Ile	Phe	Ser	His	Tyr	Ala	Thr	Gly	Ile	Asn
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Phe	Asp	Lys	Tyr	Asp	Asp	Ile	Leu	Val	Asp	Val	Ser	Gly	Ser	Asn	Pro
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			260				265						270		
Ser	Lys	Asn	Val	Ser	Lys	Ser	Gly	Tyr	Val	Lys	Pro	Thr	Pro	Val	Gln
		275					280					285			
Lys	His	Gly	Ile	Pro	Ile	Ile	Ser	Ala	Gly	Arg	Asp	Leu	Met	Ala	Cys
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Gln	Arg	Phe	Met	Thr	Asp	Gly	Val	Ala	Ala	Ser	Lys	Phe	Ser	Glu	Ile
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Gln	Glu	Pro	Glu	Ala	Ile	Ile	Val	Ala	Pro	Thr	Arg	Glu	Leu	Ile	Asn
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Pro	Val	Val	Val	Tyr	Gly	Gly	Ile	Asn	Thr	Gly	Tyr	Thr	Ile	Arg	Glu
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Val	Leu	Lys	Gly	Cys	Asn	Val	Leu	Cys	Ala	Thr	Pro	Gly	Arg	Leu	His
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Asp	Leu	Ile	Gly	Arg	Gly	Lys	Ile	Gly	Leu	Ser	Lys	Val	Arg	Tyr	Leu
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Val	Leu	Asp	Glu	Ala	Asp	Arg	Met	Leu	Asp	Met	Gly	Phe	Glu	Pro	Glu
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Met	Arg	Lys	Leu	Val	Ala	Ser	Pro	Gly	Met	Pro	Ser	Lys	Glu	Lys	Arg
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Ala	Ala	Asp	Phe	Leu	Lys	Val	Asp	Tyr	Ile	Phe	Leu	Ala	Val	Gly	Val
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Val	Gly	Gly	Ala	Cys	Ser	Asp	Val	Glu	Gln	Thr	Ile	Val	Gln	Val	Asp
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Gln	Tyr	Ser	Lys	Arg	Asp	Gln	Leu	Leu	Glu	Leu	Leu	Arg	Ala	Thr	Gly
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E

440

Asn	Glu	Arg	Thr	Met	Val	Phe	Val	Glu	Thr	Lys	Arg	Ser	Ala	Asp	Phe
		515					520					525			
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Leu	Gly	His	Cys	Pro	Val	Leu	Val	Ala	Thr	Ser	Val	Ala	Ala	Arg	Gly
			565						570					575	
Leu	Asp	Ile	Glu	Gln	Val	Gln	His	Val	Val	Asn	Phe	Asp	Met	Pro	Ser
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		595					600					605			
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Leu	Ala	Arg	Ser	Leu	Val	Lys	Val	Leu	Ser	Gly	Ala	Gln	Gln	Val	Val
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Pro	Lys	Trp	Leu	Glu	Glu	Val	Ala	Phe	Ser	Ala	His	Gly	Thr	Thr	Gly
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Phe	Asn	Pro	Arg	Gly	Lys	Val	Phe	Ala	Ser	Thr	Asp	Ser	Arg	Lys	Gly
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Gly	Glu	Ala	Glu	Gly	Asp	Gly	Val	Gly	Gly	Ser	Gly	Gly	Glu	Gly	Gly
		35					40						45		
Gly	Tyr	Gln	Gly	Gly	Asn	Arg	Asp	Val	Phe	Gly	Arg	Ile	Gly	Gly	Gly
	50				55						60				
Arg	Gly	Gly	Gly	Ala	Gly	Gly	Tyr	Arg	Gly	Gly	Asn	Arg	Asp	Gly	Gly
65					70					75				80	
Gly	Phe	His	Gly	Gly	Arg	Arg	Glu	Gly	Glu	Arg	Asp	Phe	Arg	Gly	Gly
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Glu	Gly	Gly	Phe	Arg	Gly	Gly	Gln	Gly	Gly	Ser	Arg	Gly	Gly	Gln	Gly
			100					105						110	
Gly	Ser	Arg	Gly	Gly	Gln	Gly	Gly	Phe	Arg	Gly	Gly	Glu	Gly	Gly	Phe
		115					120					125			
Arg	Gly	Arg	Leu	Tyr	Glu	Asn	Glu	Asp	Gly	Asp	Glu	Arg	Arg	Gly	Arg
		130				135					140				
Leu	Asp	Arg	Glu	Glu	Arg	Gly	Gly	Glu	Arg	Arg	Gly	Arg	Leu	Asp	Arg
145					150				155					160	
Glu	Glu	Arg	Gly	Gly	Glu	Arg	Gly	Glu	Arg	Gly	Asp	Gly	Gly	Phe	Ala
				165					170					175	
Arg	Arg	Arg	Arg	Asn	Glu	Asp	Asp	Ile	Asn	Asn	Asn	Asn	Asn	Ile	Ala
			180					185						190	
Glu	Asp	Val	Glu	Arg	Lys	Arg	Glu	Phe	Tyr	Ile	Pro	Pro	Glu	Pro	Ser
		195					200						205		
Asn	Asp	Ala	Ile	Glu	Ile	Phe	Ser	Ser	Gly	Ile	Ala	Ser	Gly	Ile	His

*appears to be*  
 CA 72 735

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Phe Ser Lys Tyr Asn Asn Ile Pro Val Lys Val Thr Gly Ser Asp Val				
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Pro Gln Pro Ile Gln His Phe Thr Ser Ala Asp Leu Arg Asp Ile Ile				
	245		250	255
Ile Asp Asn Val Asn Lys Ser Gly Phe Lys Ile Pro Thr Pro Ile Gln				
	260		265	270
Lys Cys Ser Ile Pro Val Ile Ser Ser Gly Arg Asp Leu Met Ala Cys				
	275		280	285
Ala Gln Thr Gly Ser Gly Lys Thr Ala Ala Phe Leu Leu Pro Ile Leu				
	290		295	300
Ser Lys Leu Leu Glu Asp Pro His Glu Leu Glu Leu Gly Arg Pro Gln				
305		310		320
Val Val Ile Val Ser Pro Thr Arg Glu Leu Ala Ile Gln Ile Phe Asn				
	325		330	335
Glu Ala Arg Lys Phe Ala Phe Glu Ser Tyr Leu Lys Ile Gly Ile Val				
	340		345	350
Tyr Gly Gly Thr Ser Phe Arg His Gln Asn Glu Cys Ile Thr Arg Gly				
	355		360	365
Cys His Val Val Ile Ala Thr Pro Gly Arg Leu Leu Asp Phe Val Asp				
	370		375	380
Arg Thr Phe Ile Thr Phe Glu Asp Thr Arg Phe Val Val Leu Asp Glu				
385		390		400
Ala Asp Arg Met Leu Asp Met Gly Phe Ser Glu Asp Met Arg Arg Ile				
	405		410	415
Met Thr His Val Thr Met Arg Pro Glu His Gln Thr Leu Met Phe Ser				
	420		425	430
Ala Thr Phe Pro Glu Glu Ile Gln Arg Met Ala Gly Glu Phe Leu Lys				
	435		440	445
Asn Tyr Val Ser Val Ala Ile Gly Ile Val Gly Gly Ala Cys Ser Asp				
	450		455	460
Val Lys Gln Thr Ile Tyr Glu Val Asn Lys Tyr Ala Lys Arg Ser Lys				
465		470		480
Leu Ile Glu Ile Leu Ser Glu Gln Ala Asp Gly Thr Ile Val Phe Val				
	485		490	495
Glu Thr Lys Arg Gly Ala Asp Phe Leu Ala Ser Phe Leu Ser Glu Lys				
	500		505	510
Glu Phe Pro Thr Thr Ser Ile His Gly Asp Arg Leu Gln Ser Gln Arg				
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Ala Thr Ser Val Ala Ser Arg Gly Leu Asp Ile Lys Asn Ile Lys His				
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Ile Gly Arg Thr Gly Cys Val Gly Asn Asn Gly Arg Ala Thr Ser Phe				
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Phe Asp Pro Glu Lys Asp Arg Ala Ile Ala Ala Asp Leu Val Lys Ile				
	595		600	605
Leu Glu Gly Ser Gly Gln Thr Val Pro Asp Phe Leu Arg Thr Cys Gly				
	610		615	620
Ala Gly Gly Asp Gly Gly Tyr Ser Asn Gln Asn Phe Gly Gly Val Asp				
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Glu Glu Gln Trp Asp				
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28

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gcttcagggc catacagaag aggtggaaga ggtagtttcc gaggttgccg tggaggattt 480  
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